STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number:	10/530,106
Source:	PUTIO
Date Processed by STIC:	4/12/05
2	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

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- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
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Revised 01/24/05



PCT

RAW SEQUENCE LISTING DATE: 04/12/2005 PATENT APPLICATION: US/10/530,106 TIME: 10:20:31

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04122005\J530106.raw

```
5 <110 > APPLICANT: Hooft Van Huijsduijnen, Rob
```

Walchli, Sebastien

9 <120> TITLE OF INVENTION: Use of protein tyrosine phosphatase inhibitors for prevention and/or

treatment of cancer

14 <130> FILE REFERENCE: SLII-P01-003

C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/530,106

C--> 17 <141> CURRENT FILING DATE: 2005-04-01

17 <160> NUMBER OF SEQ ID NOS: 34

21 <170> SOFTWARE: PatentIn version 3.1

25 <210> SEQ ID NO: 1

27 <211> LENGTH: 1115

29 <212> TYPE: PRT

31 <213> ORGANISM: Homo sapiens

35 <400> SEQUENCE: 1

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45 Gly Arg Asn Leu Thr Val Glu Thr Gln Thr Thr Ser Ser Ile Ser Leu

49 Ser Trp Glu Val Pro Asp Gly Leu Asp Ser Gln Asn Ser Asn Tyr Trp

53 Val Gln Cys Thr Gly Asp Gly Gly Thr Thr Glu Thr Arg Asn Thr Thr 75

57 Ala Thr Asn Val Thr Val Asp Gly Leu Gly Pro Gly Ser Leu Tyr Thr

61 Cys Ser Val Trp Val Glu Lys Asp Gly Val Asn Ser Ser Val Gly Thr 100 105

65 Val Thr Thr Ala Thr Ala Pro Asn Pro Val Arg Asn Leu Arg Val Glu

115 120

69 Ala Gln Thr Asn Ser Ser Ile Ala Leu Thr Trp Glu Val Pro Asp Gly 130 135 140

73 Pro Asp Pro Gln Asn Ser Thr Tyr Gly Val Glu Tyr Thr Gly Asp Gly 150

77 Gly Arg Ala Gly Thr Arg Ser Thr Ala His Thr Asn Ile Thr Val Asp

165 170

81 Gly Leu Glu Pro Gly Cys Leu Tyr Ala Phe Ser Met Trp Val Gly Lys 180 185

85 Asn Gly Ile Asn Ser Ser Arg Glu Thr Arg Asn Ala Thr Thr Ala His

200 89 Asn Pro Val Arg Asn Leu Arg Val Glu Ala Gln Thr Thr Ser Ser Ile

210 215

93 Ser Leu Ser Trp Glu Val Pro Asp Gly Thr Asp Pro Gln Asn Ser Thr

Jerrected Diskette Needer pp 6-7





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Input Set : A:\pto.da.txt

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94 2	225				:	230				:	235				2	240
97 7	fyr (Cys :	[le (Gln (Cys :	Thr (3ly A	Asp (Gly (Gly A	Arg :	Thr (Glu :	Thr A	Arg A	Asn
98					245					250					255	
101	Thr	Thr	Asp		Arg	Val	Thr	Val		Gly	Leu	Gly	Pro	Gly	Ser	Leu
102				260				_	265		_			270		_
	Tyr	Thr	_	Ser	Val	Trp	Val		Lys	Asp	Gly	Val		Ser	Ser	Val
106	_		275					280	_	_	_		285		_	
	Glu		Val	Thr	Ser	Thr		Ala	Pro	Asn	Pro		Arg	Asn	Leu	Thr
110		290				_	295	_			_	300	_			_
		GIu	Ala	Gin	Thr		Ser	Ser	He	Ala		Thr	Trp	Glu	vaı	
	305	~ 1	D		D	310	3	0	m1	m	315	**- 7	~1	m	ml	320
	Asp	GIA	Pro	Asp		GIN	Asn	ser	Thr	330	GIY	vaı	GIU	Tyr		GIY
118	7	a 1	al	7	325	a1	mla so	7	C		7.7.	111.	mb	7 ~~	335	mb w
	Asp	GIA	GIY	340	Ala	Gry	1111	Arg	345	TIIL	Ala	птъ	1111	Asn 350	116	IIII
122	V-1	7 cn	Λrα		Clu	Dro	Clv	Cvc		Tur	V-1	Dhe	Cor	Val	ሞፖካ	Val
126	vai	Asp	355	пеп	GIU	FIU	GIY	360	пец	ıyı	vaı	FIIC	365	vaı	пр	Vai
	Glv	Lve		Glv	Tl۵	Δen	Ser		Δra	Glu	Thr	Δra		Ala	Thr	Thr
132	OL,	370	11511	O _T	110	11.511	375	JCI	****9	OLU	****	380	11011	1114		
	Ala		Asn	Pro	Val	Ara		Leu	His	Met	Glu		Gln	Thr	Asn	Ser
	385					390					395		U			400
		Ile	Ala	Leu	Cys		Glu	Val	Pro	Asp		Pro	Tyr	Pro	Gln	Asp
140					405	F				410	•		4		415	-
143	Tyr	Thr	Tyr	Trp	Val	Glu	Tyr	Thr	Gly	Asp	Gly	Gly	Gly	Thr	Glu	Thr
144	•		-	420			-		425		_	_	_	430		
147	Arg	Asn	Thr	Thr	Asn	Thr	Ser	Val	Thr	Ala	Glu	Arg	Leu	Glu	Pro	Gly
148			435					440					445			
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152		450					455					460				
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156						470					475					480
	Leu	Ser	Lys	Gln		\mathtt{Trp}	Thr	Asn	Ser		Ile	Ala	Leu	Arg		Thr
160			~ 7	~-3	485		~-	_	_	490	_		_		495	_
	Ala	Pro	GIn	_	Pro	GLY	GIn	Ser		Tyr	Ser	Tyr	Trp	Val	Ser	Trp
164	77-7	7	a 1	500	Ma.h	mla aa	7	D	505	ml	a1	0	mla sa	510	a 1	mb
	vai	Arg	515	GIA	мес	Thr	Asp		Arg	THE	GIII	ser		Ser	GIY	Int
168	7.00	T10		T 011	Tva	Clu	T 011	520	71-	C1++	cor	T 011	525	His	Tou	Thr
172	Asp	530	TIIL	Leu	пåр	GIU	535	Giu	міа	Gry	ser	540	TYL	піз	Бец	IIII
	Val		Δla	Glu	Δra	Δen		Val	Δra	Glv	ጥኒ/ዮ		Ser	Thr	T.e11	Thr
176		ııp	AIU	Olu	m 9	550	Olu	VUI	my	Gry	555	ADII	JCI	1111	DCu.	560
		Ala	Thr	Ala	Pro		Glu	Val	Thr	Asp		Gln	Asn	Glu	Thr	
180					565					570		~			575	
	Thr	Lvs	Asn	Ser		Met	Leu	Trp	Trp		Ala	Pro	Glv	Asp		His
184		2 =		580				- E	585	4 .			- 1	590		•
	Ser	Gln	Leu		Val	Tyr	Trp	Val		Trp	Ala	Ser	Lys	Gly	His	Pro
188			595	-		-	-	600		-			605	•		
191	Arg	Arg	Gly	Gln	Asp	Pro	Gln	Ala	Asn	Trp	Val	Asn	Gln	Thr	Ser	Arg
192	-	610	=		_		615					620				



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	625 Tyr	Asn	Phe	Thr	Val	630 Trp	Ala	Glu	Arg	Asn	635 Asp	Val	Ala	Ser	Ser	640 Thr
200	4				645	-				650	-				655	
203 204	Gln	Ser	Leu	Cys 660	Ala	Ser	Thr	Tyr	Pro 665	Asp	Thr	Val	Thr	Ile 670	Thr	Ser
207	Cys	Val			Ser	Ala	Gly	_	_	Val	Asn	Leu	Ile 685		Ser	Cys
208	Pro	Gln	675	Glv	Tur	Glu	Δla	680 Phe	Glu	T.em	Glu	Val		Glv	Gln	Ara
212		690	-	-	-		695					700	_	_		_
	Gly	Ser	Gln	Asp	Arg		Ser	Cys	Gly	Glu		Val	Ser	Val	Leu	
	705	~1	_			710		n	- 1 -	m1	715	m1	m1	- 1 -	m	720
219	Leu	GIY	Pro	Ala	725	ser	туr	Pro	Ala	730	11e	Tnr	Thr	11e	735	Asp
223	Gly	Met	Lys	Val	Val	Ser	His	Ser		Val	Cys	His	Thr	Glu	Ser	Ala
224				740					745					750	_	
227 228	Gly	Val	Ile 755	Ala	Gly	Ala	Phe	Val 760	Gly	Ile	Leu	Leu	Phe 765	Leu	Ile	Leu
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	785					790					795					800
239	Pro	Ala	Glu	Asp	Phe	Ala	Asp	His	Val	Arg	Lys	Asn	Glu	Arg	Asp	Ser
240					805					810					815	
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244	_		_	820				_	825	_	~7	_	_	830	_	_
	Ser	GIn			Met	Val	Ala		Ala	Ser	GIu	Asn		Ala	ьys	Asn
248	Arg	M	835		1707	T 011	Dwo	840	7 ~~	TT-ww	Cox	7 ~~~	845	Dro	T 011	T ***
251	Arg	850	Arg	ASII	vai	Leu	855	ıyı	АБР	пр	ser	860	vaı	PLO	пеп	пуъ
	Pro		Hic	Glu	Glu	Pro		Ser	Asn	Tyr	Tle		Δla	Ser	Phe	Met
	865			014	014	870	017	001	1100	~] ~	875					880
	Pro	Gly	Leu	Trp	Ser		Gln	Glu	Phe	Ile		Thr	Gln	Gly	Pro	Leu
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263	Pro	Gln	Thr	Val	Gly	Asp	Phe	Trp	Arg	Leu	Val	Trp	Glu	Gln	Gln	Ser
264				900					905					910		
267	His	Thr	Leu	Val	Met	Leu	Thr		Cys	Met	Glu	Ala	Gly	Arg	Val	Lys
268			915					920					925		- · -	
	Cys													His	Gly	His
	•													(T)	mla	17-7
	Leu	Arg	vaı	Tnr	ьeu		GIY	GIU	GIU	vaı		GIU	Asn	Trp	Thr	960
	945 Arg	C1	Τ	T 011	T 011	950	Cln	W-1	Clu	C1.,	955	Tvo	Thr	LON	cor	
280	ALG	GIU	ьеи	neu	965	пеп	GIII	vaı	GIU	970	GIII	пув	TIIT	neu	975	Val
	Arg	Gln	Phe	ніс		Glp	Δla	ሞፖጥ	Pro		Hic	Glv	Val	Pro		Ser
284	n. g	0111	1116	980	- y -	0111	1114	111	985	nap	1113	O ± y	VUI	990	JCI	501
	Pro	Asp	Thr		Leu	Ala	Phe	Trp		n Mei	t Lei	ı Ard	ı Glı		co Le	eu Asp
288			995					1000		,		:	100		·	P
		Gln Thr Met Glu Gly Gly Pro Pro Ile Val His Cys Ser Ala Gly										3ly				





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Input Set : A:\pto.da.txt

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1015										
292 1010 1015 1020										
295 Val Gly Arg Thr Gly Thr Leu Ile Ala Leu Asp Val Leu Leu Arg										
296 1025 1030 1035										
299 Gln Leu Gln Ser Glu Gly Leu Leu Gly Pro Phe Ser Phe Val Arg										
300 1040 1045 1050										
303 Lys Met Arg Glu Ser Arg Pro Leu Met Val Gln Thr Glu Ala Gln										
304 1055 1060 1065										
307 Tyr Val Phe Leu His Gln Cys Ile Leu Arg Phe Leu Gln Gln Ser										
308 1070 1075 1080										
311 Ala Gln Ala Pro Ala Glu Lys Glu Val Pro Tyr Glu Asp Val Glu										
312 1085 1090 1095										
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319 Glu Val										
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61 <211> LENGTH: 20										
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365 <213> ORGANISM: Artificial Sequence										
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371 <223> OTHER INFORMATION: Primer										
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Input Set : A:\pto.da.txt

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- 405 <220> FEATURE:
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- 431 <210> SEQ ID NO: 8
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- 445 <400> SEQUENCE: 8
- 446 gatgggattt ccattgatga ca 22
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- 455 <213> ORGANISM: Artificial Sequence
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- 477 <220> FEATURE:
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- 482 cctagtccca gggctttgat t
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- 487 <211> LENGTH: 22
- 489 <212> TYPE: DNA
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10/530,106 6

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<211> 20

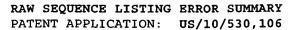
<212> DNA

· <213> Artificial sequence

needs explanation - see p. 7

<400> 32 gcgcgctagc cacttcggaa

20



DATE: 04/12/2005 TIME: 10:20:32

Input Set : A:\pto.da.txt

enn Splanton Output Set: N:\CRF4\04122005\J530106.raw

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings. Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or"Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seg#:32



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Input Set : A:\pto.da.txt

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:879 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>

ORGANISM: Artificial sequence

L:879 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>

ORGANISM: Artificial sequence

L:879 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32, Line#:879